

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

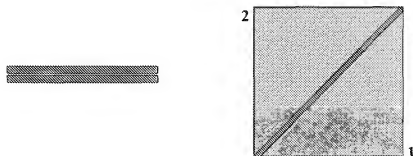
Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **0** expect: **10.000** wordsize: **3** Filter ☐ View option: **Standard**
 Masking character option: **X for protein, n for nucleotide** Masking color option: **Black**
☐ Show CDS translation **Align**

Sequence 1: results for sequence "sin2" starting "AspIleValMet"

Length = 108 (1 .. 108)

Sequence 2: results for sequence "sin4" starting "AspIleLeuMet"

Length = 108 (1 .. 108)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

```

Score = 178 bits (452), Expect = 9e-44
Identities = 86/108 (79%), Positives = 96/108 (88%), Gaps = 0/108 (0%)

Query 1  DIVMTQSHKFMSTSVGDRVSITOKASQDVSTAVAWYQQKPGQSPFKLLIYSASYRYTGVP 60
          DI+MTQS KFMSTSVGDRVS+TKASQ+V VAWYQQKPGQSPK LIYSASYRY+GVP
Sbjct 1  DILMTQSQKFMSTSVGDRVSVTCASQNVGINVAVYQQKPGQSPKALIIYSASYRYSEVPD 60

Query 61  RFGSGSGTDFTFTISSVQTEDLAVYYCQOHYRTPTPTFGGGTKLELKR 108
          RF+GSGSGTDFT TIS+VQ+EDLA Y+COQ+ P TFGGGTKLE+KR
Sbjct 61  RFTGSGSGTDFTLTISNVQSEDLAEYFCQYNSYPLTFTFGGGTKLEIKR 108
          C.D.L.3

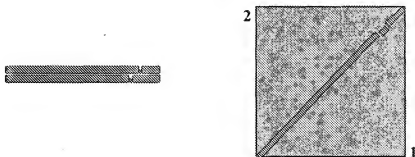
CPU time:      0.05 user secs.      0.03 sys. secs      0.08 total secs.
  
```

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☐ Show CDS translation **Align**

Sequence 1: results for sequence "sin1" starting "GlnValGlnLeu"
 Length = 120 (1 .. 120)

Sequence 2: results for sequence "sin3" starting "GlnValGlnLeu"
 Length = 119 (1 .. 119)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 157 bits (396), Expect = 3e-37
 Identities = 79/122 (64%), Positives = 94/122 (77%), Gaps = 5/122 (4%)

Query	1	QVQLKQSGAELVRFPGASVRLSCKASGYTFT	CDL1	QVQLKQSGAELVRFPGASVRLSCKASGYTFT	CDL2	60
		QVQL+QSG EL +PGASV++SCKASGY+F+ Y +NM+KQ + LEWIG IDPY+ +T Y				
Sbjct	1	QVQLKQSGPELEKPGASVKISCKASGYSPSYNMN		QVQLKQSGPELEKPGASVKISCKASGYSPSYNMN		60
Query	61	NQKFKDRAILTVDKYSSTAYMQLSSLTSEDSAVYYCAR	CDL1	NQKFKDRAILTVDKYSSTAYMQLSSLTSEDSAVYYCAR	CDL2	118
		NQKFK KA LT+DK SSTAYMQL SLTSEDSAVY+CA+ W F WG GT VIV				
Sbjct	61	NQKFKGKATLTLDKSSSTAYMQLKSLTSEDSAVYFCAR		NQKFKGKATLTLDKSSSTAYMQLKSLTSEDSAVYFCAR		117
Query	119	SS 120				
		S+ 119				
Sbjct	118	SA 119				

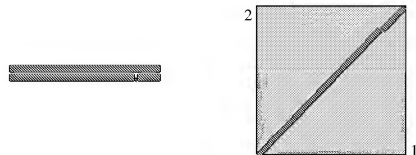
CPU time: 0.04 user secs. 0.04 sys. secs 0.08 total secs.

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Matrix: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter: ☐ View option:
 Masking character option: Masking color option:
☐ Show CDS translation

Sequence 1: results for sequence "sin7" starting "GlnValGlnLeu"
 Length = 119 (1 .. 119)

Sequence 2: results for sequence "sin25" starting "GluValGlnLeu"
 Length = 117 (1 .. 117)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 159 bits (402), Expect = 6e-38

Identities = 77/119 (64%), Positives = 95/119 (79%), Gaps = 2/119 (1%)

```

Query 1 QVQLQQSGGELVRPGTISVKVCKASGYAFTNYLIEWIRQRPGQGLEWIGVINPGSGNSKS 60
+VQLQQSG ELVRPG SVK+SCK S Y FT+Y + W++Q + LEWIGVI+ GN K
Sbjct 1 EVQLQQSGPELVRPGSVKISCKGSSYKFTDYAMHWVKQSHAKSLEWIGVISTYYGNV KY 60

Query 61 SKNLKGKATLTADKSSNTAYMQLSSLTSDSAVYFCARSGVGYGSSPDYWGQGTITLVSS 119
++ FGKAT+T DKSS+TAYM+L+ LTS+DSAVY+CARS YGS DYWGQGT++TVSS
Sbjct 61 NQKFKGKATMTVDKSSSTAYMELARLTSDSAVYVCARS--YGSYLDYWGQGTSTVSS 117
    
```

CPU time: 0.04 user secs.

0.04 sys. secs

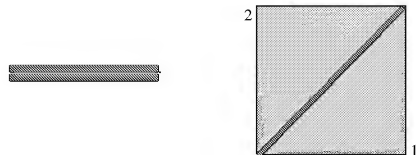
0.08 total secs.

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 x_dropoff: expect: wordsize: Filter: ☐ View option:
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Sequence 1: results for sequence "sin8" starting "AspValValMet"
 Length = 113 (1 .. 113)

Sequence 2: results for sequence "sin26" starting "AspIleValMet"
 Length = 112 (1 .. 112)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 227 bits (579), Expect = 2e-58
 Identities = 110/112 (98%), Positives = 111/112 (99%), Gaps = 0/112 (0%)

```

Query 1 DVVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQGSPKRLIYLVSKLD 60
      D+VMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQGSPKRLIYLVSKLD 60
Sbjct 1 DIVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQGSPKRLIYLVSKLD 60

Query 61 SGVPDRFTGSGSGDTFTLKISRVEAEDLGVYYCWQGHFPTFGGGTKLEIK 112
      SGVPDRFTGSGSGDTFTLKISRVEAEDLGVYYCWQGHFPTFGGGTKLEIK 112
Sbjct 61 SGVPDRFTGSGSGDTFTLKISRVEAEDLGVYYCWQGHFPTFGGGTKLEIK 112
    
```

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.